TEAM 1

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RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/586,594B*

DATE: 11/19/96
TIME: 11:49:51

INPUT SET: S13874.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

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 1                              SEQUENCE LISTING
 2
 3    (1)    General Information:
 4
 5       (i) APPLICANT: Friedman, Jeffrey M.
 6                      Lee, Gwo-Hua
 7                      Proenca, Ricardo
 8
 9      (ii) TITLE OF INVENTION: DB, THE RECEPTOR FOR LEPTIN, NUCLEIC
10              ACIDS ENCODING THE RECEPTOR, AND USES THEREOF
11
12     (iii) NUMBER OF SEQUENCES: 54
13
14      (iv) CORRESPONDENCE ADDRESS:
15           (A) ADDRESSEE: David A. Jackson, Esq.
16           (B) STREET: 411 Hackensack Ave, Continental Plaza, 4th
17                  Floor
18           (C) CITY: Hackensack
19           (D) STATE: New Jersey
20           (E) COUNTRY: USA
21           (F) ZIP: 07601
22
23       (v) COMPUTER READABLE FORM:
24           (A) MEDIUM TYPE: Floppy disk
25           (B) COMPUTER: IBM PC compatible
26           (C) OPERATING SYSTEM: PC-DOS/MS-DOS
27           (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
28
29      (vi) CURRENT APPLICATION DATA:
30           (A) APPLICATION NUMBER: US 08/586,594
31           (B) FILING DATE:
32           (C) CLASSIFICATION:
33
34    (viii) ATTORNEY/AGENT INFORMATION:
35           (A) NAME: Jackson Esq., David A.
36           (B) REGISTRATION NUMBER: 26,742
37           (C) REFERENCE/DOCKET NUMBER: 600-1-162
38
39      (ix) TELECOMMUNICATION INFORMATION:
40           (A) TELEPHONE: 201-487-5800
41           (B) TELEFAX: 201-343-1684
42
43
44    (2) INFORMATION FOR SEQ ID NO:1:
45
46       (i) SEQUENCE CHARACTERISTICS:
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47              (A) LENGTH: 2529 base pairs
48              (B) TYPE: nucleic acid
49              (C) STRANDEDNESS: double
50              (D) TOPOLOGY: linear
51
52        (ii) MOLECULE TYPE: cDNA
53
54        (iii) HYPOTHETICAL: NO
55
56        (iv) ANTI-SENSE: NO
57
58
59        (vii) IMMEDIATE SOURCE:
60              (B) CLONE: A15 (OB-Ra)
61
62
63
64        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
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66  GGGCTCAGGT CGGCGTCGTA CCAGCCGCTG AAGCGGTTCT CCAGGTTCCA GGCGCTCTCG        60
67
68  CCATGCCGGA TCAGCACCAG CTTGTAGCTC GTGCCGAATT CGGCACGAGG TTGCTTTGGG       120
69
70  AATGAGCAAG GTCAAAACTG CTCTGCACTC ACAGACAACA CTGAAGGGAA GACACTGGCT       180
71
72  TCAGTAGTGA AGGCTTCAGT TTTTCGCCAG CTAGGTGTAA ACTGGGACAT AGAGTGCTGG       240
73
74  ATGAAAGGGG ACTTGACATT ATTCATCTGT CATATGGAGC CATTACCTAA GAACCCCTTC       300
75
76  AAGAATTATG ACTCTAAGGT CCATCTTTTA TATGATCTGC CTGAAGTCAT AGATGATTCG       360
77
78  CCTCTGCCCC CACTGAAAGA CAGCTTTCAG ACTGTCCAAT GCAACTGCAG TCTTCGGGGA       420
79
80  TGTGAATGTC ATGTGCCGGT ACCCAGAGCC AAACTCAACT ACGCTCTTCT GATGTATTTG       480
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82  GAAATCACAT CTGCCGGTGT GAGTTTTCAG TCACCTCTGA TGTCACTGCA GCCCATGCTT       540
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84  GTTGTGAAAC CCGATCCACC CTTAGGTTTG CATATGGAAG TCACAGATGA TGGTAATTTA       600
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86  AAGATTTCTT GGGACAGCCA AACAATGGCA CCATTTCCGC TTCAATATCA GGTGAAATAT       660
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88  TTAGAGAATT CTACAATTGT AAGAGAGGCT GCTGAAATTG TCTCAGCTAC ATCTCTGCTG       720
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90  GTAGACAGTG TGCTTCCTGG ATCTTCATAT GAGGTCCAGG TGAGGAGCAA GAGACTGGAT       780
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92  GGTTCAGGAG TCTGGAGTGA CTGGAGTTCA CCTCAAGTCT TTACCACACA AGATGTTGTG       840
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94  TATTTTCCAC CCAAAATTCT GACTAGTGTT GGATCGAATG CTTCTTTTCA TTGCATCTAC       900
95
96  AAAAACGAAA ACCAGATTAT CTCCTCAAAA CAGATAGTTT GGTGGAGGAA TCTAGCTGAG       960
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98  AAATCCCTG AGATACAGTA CAGCATTGTG AGTGACCGAG TTAGCAAAGT TACCTTCTCC      1020
99
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INPUT SET: S13874.raw

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102    GAGCAGGCGT GCCATCACCG CTATGCTGAA TTATACGTGA TCGATGTCAA TATCAATATA    1140
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104    TCATGTGAAA CTGACGGGTA CTTAACTAAA ATGACTTGCA GATGGTCACC CAGCACAATC    1200
105
106    CAATCACTAG TGGGAAGCAC TGTGCAGCTG AGGTATCACA GGCGCAGCCT GTATTGTCCT    1260
107
108    GATAGTCCAT CTATTCATCC TACGTCTGAG CCCAAAAACT GCGTCTTACA GAGAGACGGC    1320
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110    TTTTATGAAT GTGTTTTCCA GCCAATCTTT CTATTATCTG CTATACAAT  GTGGATCAGG    1380
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112    ATCAACCATT CTTTAGGTTC ACTTGACTCG CCACCAACGT GTGTCCTTCC TGACTCCGTA    1440
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114    GTAAAACCAC TACCTCCATC TAACGTAAAA GCAGAGATTA CTGTAAACAC TGGATTATTG    1500
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116    AAAGTATCTT GGGAAAAGCC AGTCTTTCCG GAGAATAACC TTCAATTCCA GATTCGATAT    1560
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118    GGCTTAAGTG GAAAAGAAAT ACAATGGAAG ACACATGAGG TATTCGATGC AAAGTCAAAG    1620
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120    TCTGCCAGCC TGCTGGTGTC AGACCTCTGT GCAGTCTATG TGGTCCAGGT TCGCTGCCGG    1680
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122    CGGTTGGATG GACTAGGATA TTGGAGTAAT TGGAGCAGTC CAGCCTATAC GCTTGTCATG    1740
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124    GATGTAAAAG TTCCTATGAG AGGGCCTGAA TTTTGGAGAA AAATGGATGG GGACGTTACT    1800
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126    AAAAAGGAGA GAAATGTCAC CTTGCTTTGG AAGCCCCTGA CGAAAAATGA CTCACTGTGT    1860
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128    AGTGTGAGGA GGTACGTGGT GAAGCATCGT ACTGCCCACA ATGGGACGTG GTCAGAAGAT    1920
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130    GTGGGAAATC GGACCAATCT CACTTTCCTG TGGACAGAAC CAGCGCACAC TGTTACAGTT    1980
131
132    CTGGCTGTCA ATTCCCTCGG CGCTTCCCTT GTGAATTTTA ACCTTACCTT CTCATGGCCC    2040
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134    ATGAGTAAAG TGAGTGCTGT GGAGTCACTC AGTGCTTATC CCCTGAGCAG CAGCTGTGTC    2100
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136    ATCCTTTCCT GGACACTGTC ACCTGATGAT TATAGTCTGT TATATCTGGT TATTGAATGG    2160
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138    AAGATCCTTA ATGAAGATGA TGGAATGAAG TGGCTTAGAA TTCCCTCGAA TGTTAAAAAG    2220
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140    TTTTATATCC ACGATAATTT TATTCCCATC GAGAAATATC AGTTTAGTCT TTACCCAGTA    2280
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142    TTTATGGAAG GAGTTGGAAA ACCAAAGATA ATTAATGGTT TCACCAAAGA TGCTATCGAC    2340
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144    AAGCAGCAGA ATGACGCAGG GCTGTATGTC ATTGTACCCA TAATTATTTC CTCTTGTGTC    2400
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146    CTACTGCTCG GAACACTGTT AATTTCACAC CAGAGAATGA AAAAGTTGTT TTGGGACGAT    2460
147
148    GTTCCAAACC CCAAGAATTG TTCCTGGGCA CAAGGACTGA ATTTCCAAAA GAGAACGGAC    2520
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150    ACTCTTTGA                                                             2529
151
152    (2) INFORMATION FOR SEQ ID NO:2:
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153
154        (i) SEQUENCE CHARACTERISTICS:
155            (A) LENGTH: 842 amino acids
156            (B) TYPE: amino acid
157            (C) STRANDEDNESS: Not Relevant
158            (D) TOPOLOGY: Not Relevant
159
160       (ii) MOLECULE TYPE: protein
161
162      (iii) HYPOTHETICAL: NO
163
164       (iv) ANTI-SENSE: NO
165
166
167      (vii) IMMEDIATE SOURCE:
168            (B) CLONE: OB-Ra
169
170
171
172       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
173
174        Gly Leu Arg Ser Ala Ser Tyr Gln Pro Leu Lys Arg Phe Ser Arg Phe
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177        Gln Ala Leu Ser Pro Cys Arg Ile Ser Thr Ser Leu Xaa Leu Val Pro
178                    20                  25                  30
179
180        Asn Ser Ala Arg Gly Cys Phe Gly Asn Glu Gln Gly Gln Asn Cys Ser
181                    35                  40                  45
182
183        Ala Leu Thr Asp Asn Thr Glu Gly Lys Thr Leu Ala Ser Val Val Lys
184             50                  55                  60
185
186        Ala Ser Val Phe Arg Gln Leu Gly Val Asn Trp Asp Ile Glu Cys Trp
187        65                  70                  75                  80
188
189        Met Lys Gly Asp Leu Thr Leu Phe Ile Cys His Met Glu Pro Leu Pro
190                    85                  90                  95
191
192        Lys Asn Pro Phe Lys Asn Tyr Asp Ser Lys Val His Leu Leu Tyr Asp
193                    100                 105                 110
194
195        Leu Pro Glu Val Ile Asp Asp Ser Pro Leu Pro Pro Leu Lys Asp Ser
196             115                 120                 125
197
198        Phe Gln Thr Val Gln Cys Asn Cys Ser Leu Arg Gly Cys Glu Cys His
199             130                 135                 140
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201        Val Pro Val Pro Arg Ala Lys Leu Asn Tyr Ala Leu Leu Met Tyr Leu
202        145                 150                 155                 160
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204        Glu Ile Thr Ser Ala Gly Val Ser Phe Gln Ser Pro Leu Met Ser Leu
205                    165                 170                 175
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207   Gln Pro Met Leu Val Val Lys Pro Asp Pro Pro Leu Gly Leu His Met
208   180   185   190
209
210   Glu Val Thr Asp Asp Gly Asn Leu Lys Ile Ser Trp Asp Ser Gln Thr
211   195   200   205
212
213   Met Ala Pro Phe Pro Leu Gln Tyr Gln Val Lys Tyr Leu Glu Asn Ser
214   210   215   220
215
216   Thr Ile Val Arg Glu Ala Ala Glu Ile Val Ser Ala Thr Ser Leu Leu
217   225   230   235   240
218
219   Val Asp Ser Val Leu Pro Gly Ser Ser Tyr Glu Val Gln Val Arg Ser
220   245   250   255
221
222   Lys Arg Leu Asp Gly Ser Gly Val Trp Ser Asp Trp Ser Ser Pro Gln
223   260   265   270
224
225   Val Phe Thr Thr Gln Asp Val Val Tyr Phe Pro Pro Lys Ile Leu Thr
226   275   280   285
227
228   Ser Val Gly Ser Asn Ala Ser Phe His Cys Ile Tyr Lys Asn Glu Asn
229   290   295   300
230
231   Gln Ile Ile Ser Ser Lys Gln Ile Val Trp Trp Arg Asn Leu Ala Glu
232   305   310   315   320
233
234   Lys Ile Pro Glu Ile Gln Tyr Ser Ile Val Ser Asp Arg Val Ser Lys
235   325   330   335
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237   Val Thr Phe Ser Asn Leu Lys Ala Thr Arg Pro Arg Gly Lys Phe Thr
238   340   345   350
239
240   Tyr Asp Ala Val Tyr Cys Cys Asn Glu Gln Ala Cys His His Arg Tyr
241   355   360   365
242
243   Ala Glu Leu Tyr Val Ile Asp Val Asn Ile Asn Ile Ser Cys Glu Thr
244   370   375   380
245
246   Asp Gly Tyr Leu Thr Lys Met Thr Cys Arg Trp Ser Pro Ser Thr Ile
247   385   390   395   400
248
249   Gln Ser Leu Val Gly Ser Thr Val Gln Leu Arg Tyr His Arg Arg Ser
250   405   410   415
251
252   Leu Tyr Cys Pro Asp Ser Pro Ser Ile His Pro Thr Ser Glu Pro Lys
253   420   425   430
254
255   Asn Cys Val Leu Gln Arg Asp Gly Phe Tyr Glu Cys Val Phe Gln Pro
256   435   440   445
257
258   Ile Phe Leu Leu Ser Gly Tyr Thr Met Trp Ile Arg Ile Asn His Ser